

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions,
and listings of claims in the application:

LISTING OF CLAIMS:

1-43. (canceled)

44. (withdrawn) Mutated V1/AR1/AV1 or C1/AL1/AC1 gene sequence of a tomato infecting geminivirus wherein the mutations consist of point mutations distributed along the sequence in such a way that the continuous homology between the mutated sequence and the corresponding viral gene sequence is below or equal to 8 nucleotides, preferably below or equal to 5 nucleotides, said mutated sequence encoding for a capsid protein or for a Rep protein, respectively.

45. (withdrawn) Mutated V1/AR1/AV1 gene sequence according to claim 44, encoding for a capsid protein having sequence SEQ ID No 7.

46. (withdrawn) Mutated C1/AL1/AC1 gene sequence according to claim 44, wherein the mutation further comprises a truncation occurring at 3' terminal so that the mutated sequence encodes for a truncated Rep protein.

47. **(withdrawn)** Mutated C1/AL1 /AC1 gene sequences according to claim 46, wherein the truncated Rep proteins consist of 130 aminoacids (Rep 130) to 210 aminoacids (Rep 210).

48. **(withdrawn)** Mutated C1/AL1/AC1 gene sequence according to claim 46 encoding for Rep 210 SEQ ID No 3 or SEQ ID No 5.

49. **(withdrawn)** Mutated C1/AL1/AC1 gene sequence encoding for Rep 130 SEQ ID No 9.

50. **(withdrawn)** Mutated gene sequence according to claim 44 wherein the tomato infecting geminivirus is TYLCSV.

51. **(withdrawn)** Synthetic construct comprising an heterologous polynucleotide sequence containing in the 5'-3' direction:

a) polynucleotide sequence acting as promoter in said plant or tissue or transformed cells;

b) a non translated polynucleotide sequence positioned 5' of the encoding region;

c) a mutated gene sequence;

d) a sequence acting as transcription terminator, positioned 3' with respect to the mutated gene sequence.

52. **(withdrawn)** Expression vector comprising the construct as defined according to claim 51.

53. **(withdrawn and currently amended)** Transgenic plant, tissue or plant cells thereof, comprising in their genome a mutated gene sequence according to claim [[43]] 44.

54. **(withdrawn and currently amended)** Seed comprising in its genome a mutated gene sequence according to claim [[43]] 44.

55. **(currently amended)** A method for the preparation of transgenic plants, plant tissue or cells thereof having long lasting resistance against geminiviruses, including the following steps:

a) ~~identification or~~ selection of a geminivirus gene-derived sequence encoding an amino acid sequence ~~able to confer~~ capable of conferring resistance against geminiviruses, said resistance being overcome over time by geminivirus induced post-transcriptional transgene silencing;

b) mutagenesis of the geminivirus gene-derived sequence, wherein the mutations consist of silent point mutations distributed along the geminivirus gene-derived sequence so that continuous homology between the mutated ~~sequences~~ sequence and the corresponding viral gene sequence is less than or equal to 8 nucleotides ~~or less than or equal to 5 nucleotides~~; and

c) insertion of the geminivirus ~~gene~~ gene-derived sequence mutated in the step b) in the plant, plant tissue or cell

thereof, using a construct comprising an heterologous polynucleotide sequence containing in the 5'-3' direction:

i) a polynucleotide sequence acting as a promoter in said plant, ~~[[or]] plant~~ tissue or ~~transformed~~ cells;

ii) a non-translated polynucleotide sequence positioned 5' of the encoding region of the geminivirus gene-derived sequence;

iii) a polynucleotide sequence encoding a mutagenised geminivirus-derived amino acid sequence, ~~properly~~ mutagenised according to step (b) and capable to be an ineffective target of the geminivirus induced post-transcriptional ~~gene~~ transgene silencing ~~induced by the infecting geminivirus~~;

iv) a polynucleotide sequence acting as a transcription terminator positioned 3' with respect to said polynucleotide sequence encoding a mutagenised geminivirus-derived amino acid sequence.

56-57. (cancelled)

58. (previously presented) The method according to claim 55, wherein the geminiviruses are selected from the species belonging to the Begomovirus genus and isolates thereof.

59. (previously presented) The method according to claim 58, wherein the Begomoviruses species is Tomato yellow leaf curl Sardinia virus (TYLCSV).

60. (cancelled)

61. (currently amended) The method according to claim 55, wherein the ~~gene~~ geminivirus gene-derived sequence is ~~selected from the group consisting of~~ C1/AL1/AC1 belonging to TYLCSV.

62. (cancelled)

63. (currently amended) The method according to claim 61, wherein the geminivirus-derived amino acid sequence is a truncated protein with respect to the ~~viral~~ geminivirus wild-type protein.

64. (currently amended) The method according to claim 63 wherein the ~~viral gene sequences~~ geminivirus gene-derived sequence made an ineffective ~~targets~~ target of the ~~virus-induced~~ geminivirus-induced posttranscriptional ~~gene~~ transgene silencing is SEQ ID No [[8]] 4.

65. (currently amended) The method according to claim 64, wherein the truncated protein is ~~Rep-130~~ Rep-210 having the sequence of SEQ ID No [[9]] 5.

66-67. (cancelled)

68. (currently amended) The method according to claim 55, wherein the plants, plant tissues or cells thereof belong to a member selected from the group consisting of tomato, pepper, tobacco, squash, manioc, sweet potato, cotton, melon, potato, soybean, corn, wheat, sugar cane, bean, and beet.

69. (new) The method according to claim 55, wherein the continuous homology is less than or equal to 5 nucleotides.